16. The method of claim 13 wherein the amplification primer pair comprises a first primer having a sequence of SEQ ID NO:3 and a second primer having a sequence of SEQ ID NO:4.

17. The method of claim 1 wherein the method further comprises the step of counseling the subject to pursue or avoid a particular type of employment.

18. The method of claim 1 wherein the method further comprises the step of counseling the subject to avoid the environmental risk factor.

19. The method of claim 1 further comprising the step of prescribing a therapy selected from the group consisting of psychological therapy and pharmaceutical therapy.

20. The method of claim 1 wherein the method further comprises the step of prescribing an anti-depressive agent.

21. A method for discovering a conditional association between an allele of a brain-functional gene and a mental disorder phenotype, where the association is conditioned upon a pathogenic environmental risk factor status, the method comprising the steps of:

identifying at least one a mental disorder phenotype having a high or very high heritability coefficient;

identifying a pathogenic environmental risk factor that operates on the at least one phenotype via non-genetic means and having at least higher and lower risk status conditions;

ascertaining in a population of individuals an allelic profile for at least one brain-functional gene having an at-risk allele and at least one other allele; and

selecting from the at least one disorder phenotype a disorder phenotype that correlates with statistical significance in the population with the at-risk allele only under the higher risk status condition, but which lacks statistically significant correlation with the at-risk allele under the lower risk status condition, whereby the at-risk allele and the mental disorder phenotype are conditionally associated with the selected disorder phenotype, the association being conditioned upon the higher environmental risk factor status condition.

22. The method of claim 21 wherein the at-risk allele is selected from an allele of a gene expressed in a cell type known to act in the brain, a gene associated with variation in size of a brain structure, a gene associated with concentration of a neurotransmitter in the brain, a gene associated with a brain response to a stimulus as assessed by an imaging method, and a gene which when altered affect behavior of a human or non-human animal.

23. The method of claim 21 wherein the at-risk allele is an allele characterized by a short promoter allele of a 5-HTT gene.

24. The method of claim 21 wherein the mental disorder phenotype is selected from the group consisting of a behavioral disorder phenotype, an emotional disorder phenotype, and a cognitive disorder phenotype wherein genetic variation in a population accounts for a high or very high proportion of total phenotypic population variation.

25. The method of claim 21 wherein the disorder phenotype is antisocial behavior disorder.

26. The method of claim 21 wherein the disorder phenotype is depression.

27. The method of claim 21 wherein the pathogenic environmental risk factor is selected from the group consisting of exposure to psychological trauma, exposure to psychosocial stress, exposure to an unhealthy diet, an infectious agent, exposure to a toxic agent, experience with a pharmacological agent, a medical trauma, and an injury.

28. The method of claim 21 wherein the pathogenic environmental risk factor is a plurality of stressful life events.

29. The method of claim 21 wherein the pathogenic environmental risk factor is childhood maltreatment.

30. The method of claim 21 wherein the at-risk allele is an allele characterized by a short promoter allele of a 5-HTT gene, the mental disorder phenotype is depression and the pathogenic environmental risk factor is a plurality of stressful life events.

31. The method of claim 21 wherein the step of ascertaining the allelic profile comprises the steps of:

obtaining nucleic acid from the individuals in the population;

separately amplifying from the nucleic acid of the individuals a portion of the brain-functional gene using an amplification primer pair that distinguishes the at-risk allele from another allele of the brain-functional gene;

determining a genotype for the individuals regarding presence of the at-risk allele; and

classifying the genotype from individuals to ascertain the allelic profile in the population.

32. The method of claim 31 wherein the at-risk allele is characterized by a short promoter of a 5-HTT gene.

33. The method of claim 31 wherein the amplification primer pair comprises a first primer having a sequence of SEQ ID NO: 1 and a second primer having a sequence of SEQ ID NO:2.

34. A kit comprising

a questionnaire that solicits input about a subject relevant to the subject's experience with at least one of (a) a pathogenic environmental risk factor and (b) a disorder phenotype; and

a system for obtaining from the subject a sample suitable for producing an allelic profile of at least one brain-functional gene.

35. The kit of claim 34 further comprising a system for assaying the allelic profile of at least one brain-functional gene.

36. The kit of claim 35 wherein the system comprises an amplification primer pair that distinguishes the at-risk allele from another allele of the gene.

37. The kit of claim 35 wherein the at-risk allele is characterized by a short promoter of a 5-HTT gene.

38. The kit of claim 37 wherein the amplification primer pair comprises a first primer having a sequence of SEQ ID NO:3 and a second primer having a sequence of SEQ ID NO:4.

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